

## **Truly incomplete and complex chromosomal exchanges in human fibroblast cells exposed in situ to energetic heavy ions**

HONGLU WU<sup>1,\*</sup>, MARCO DURANTE<sup>2</sup>, YOSHIYA FURUSAWA<sup>3</sup>, KERRY GEORGE<sup>1</sup>, TETSUYA KAWATA<sup>4</sup> and FRANCIS A. CUCINOTTA<sup>5</sup>

<sup>1</sup>Wyle Laboratories, Houston, Texas, USA; <sup>2</sup>University of Naples, Naples, Italy; <sup>3</sup>National Institute of Radiological Sciences, Chiba, Japan; <sup>4</sup>Chiba University, Chiba, Japan and <sup>5</sup>NASA Johnson Space Center, Houston, Texas, USA

Confluent human fibroblast cells (AG1522) were irradiated with  $\gamma$  rays, 490 MeV/nucleon Si, or with Fe ions at either 200 or 500 MeV/nucleon. The cells were allowed to repair at 37 °C for 24 hours after exposure, and a chemically induced premature chromosome condensation (PCC) technique was used to condense chromosomes in the G2 phase of the cell cycle. Incomplete and complex exchanges were analyzed in the irradiated samples. In order to verify that chromosomal breaks were truly unrejoined, chromosome aberrations were analyzed using a combination of whole chromosome specific probes and probes specific for the telomere region of the chromosome. Results showed that the frequency of unrejoined chromosome breaks was higher after high-LET radiation, and consequently, the ratio of incomplete to complete exchanges increased steadily with LET up to 440 keV/ $\mu$ m, the highest LET value in the present study. For samples exposed to 200 MeV/nucleon Fe ions, chromosome aberrations were analyzed using the multicolor FISH (mFISH) technique that allows identification of both complex and truly incomplete exchanges. Results of the mFISH study showed that 0.7 and 3 Gy dose of the Fe ions produced similar ratios of complex to simple exchanges and incomplete to complete exchanges, values for which were higher than those obtained after a 6 Gy  $\gamma$  exposure. After 0.7 Gy of Fe ions, most complex aberrations were found to involve three or four chromosomes, which is a likely indication of the maximum number of chromosome domains traversed by a single Fe ion track.